



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/069,439  
Source: P5/10  
Date Processed by STIC: 3/7/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/069,439

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences  
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences  
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



PCT10

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/069,439

DATE: 03/07/2002

TIME: 15:26:54

Input Set : A:\2605-103.txt

Output Set: N:\CRF3\03072002\J069439.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: MIYATA, TOSHIO  
4 KUROKAWA, KIYOSHI  
6 <120> TITLE OF INVENTION: Meg-1 protein  
8 <130> FILE REFERENCE: 2605/103  
OK 10 <140> CURRENT APPLICATION NUMBER: US/10/069,439  
OK 11 <141> CURRENT FILING DATE: 2002-02-14  
13 <150> PRIOR APPLICATION NUMBER: PCT/JP00/05551  
15 <151> PRIOR FILING DATE: 2000-08-18  
17 <160> NUMBER OF SEQ ID NOS: 13  
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

## ERRORED SEQUENCES

600 <210> SEQ ID NO: 11  
601 <211> LENGTH: 3568 3658 shown (P.S.)  
602 <212> TYPE: DNA  
603 <213> ORGANISM: RATTUS NORVEGICUS  
605 <220> FEATURE:  
606 <221> NAME/KEY: CDS  
607 <222> LOCATION: (7)..(2862)  
609 <400> SEQUENCE: 11  
610 cacaag atg gcg gac ctc tgc ctg ctc cag gag gac ctg ccg gag gac 48  
611 Met Ala Asp Leu Ser Leu Leu Gln Glu Asp Leu Pro Glu Asp  
612 1 5 10  
614 gcg gac gga ctt ggt gtg gat gac tac agc tca gag tct gat gtg att 96  
615 Ala Asp Gly Leu Gly Val Asp Asp Tyr Ser Ser Glu Ser Asp Val Ile  
616 15 20 25 30  
618 att ata cct tca gcc ctg gac ttc gtc tca caa gat gaa atg ttg aca 144  
619 Ile Ile Pro Ser Ala Leu Asp Phe Val Ser Gln Asp Glu Met Leu Thr  
620 35 40 45  
622 ccc ttg ggg agg ctg gac aag tat gct gca agt gag aac gtc ttt aac 192  
623 Pro Leu Gly Arg Leu Asp Lys Tyr Ala Ala Ser Glu Asn Val Phe Asn  
624 50 55 60  
626 aga caa atg gtg gcc cgg agt ttg ctg gat act ctg agg gaa gtc tgt 240  
627 Arg Gln Met Val Ala Arg Ser Leu Asp Thr Leu Arg Glu Val Cys  
628 65 70 75  
630 ggt gag gag aga gac tgc att gct gtc ttg gaa agg atc agc cga ttg 288  
631 Gly Glu Glu Arg Asp Cys Ile Ala Val Leu Glu Arg Ile Ser Arg Leu  
632 80 85 90  
634 gct gat gac tca gaa cca acc gtg aga gcc gag ctg atg gaa cag gtg 336  
635 Ala Asp Asp Ser Glu Pro Thr Val Arg Ala Glu Leu Met Glu Gln Val  
636 95 100 105 110

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638	ccg	cac	atc	gca	ctg	ttt	tgt	caa	gag	aac	cga	cct	tcc	ata	cca	tat	384
639	Pro	His	Ile	Ala	Leu	Phe	Cys	Gln	Glu	Asn	Arg	Pro	Ser	Ile	Pro	Tyr	
640					115					120					125		
642	gcc	ttt	tcc	aag	tac	tta	ctg	cca	atc	gtg	gtt	aga	tac	ctt	gca	gac	432
643	Ala	Phe	Ser	Lys	Tyr	Leu	Leu	Pro	Ile	Val	Val	Arg	Tyr	Leu	Ala	Asp	
644				130					135					140			
646	cag	aat	aac	cag	gtg	agg	aaa	acc	agc	cag	gca	gct	ttg	ctg	gct	ctg	480
647	Gln	Asn	Asn	Gln	Val	Arg	Lys	Thr	Ser	Gln	Ala	Ala	Leu	Leu	Ala	Leu	
648				145					150					155			
650	ctg	gag	cag	gag	ctg	att	gag	cga	ctc	gat	gtg	gag	acc	aag	gtg	tgc	528
651	Leu	Glu	Gln	Glu	Leu	Ile	Glu	Arg	Leu	Asp	Val	Glu	Thr	Lys	Val	Cys	
652		160					165					170					
654	ccc	gtc	ctc	ata	gac	ttg	act	gcc	cca	gac	agc	aat	gac	gat	gtg	aag	576
655	Pro	Val	Leu	Ile	Asp	Leu	Thr	Ala	Pro	Asp	Ser	Asn	Asp	Asp	Val	Lys	
656	175					180					185				190		
658	aca	gag	gcc	gtg	gct	ata	atg	tgc	aag	atg	gcc	ccc	atg	gtt	ggg	aaa	624
659	Thr	Glu	Ala	Val	Ala	Ile	Met	Cys	Lys	Met	Ala	Pro	Met	Val	Gly	Lys	
660				195						200				205			
662	gat	att	aca	gag	cgt	ctc	atc	ctc	cct	agg	ttt	tgt	gag	atg	tgc	tgt	672
663	Asp	Ile	Thr	Glu	Arg	Leu	Ile	Leu	Pro	Arg	Phe	Cys	Glu	Met	Cys	Cys	
664				210					215					220			
666	gac	tgt	aga	atg	ttt	cac	gtc	cga	aag	gtc	tgt	gct	gcc	aat	ttt	gga	720
667	Asp	Cys	Arg	Met	Phe	His	Val	Arg	Lys	Val	Cys	Ala	Ala	Asn	Phe	Gly	
668			225					230					235				
670	gac	att	tgc	agc	gta	gtt	ggc	cag	caa	gct	aca	gaa	gaa	atg	ctg	ctg	768
671	Asp	Ile	Cys	Ser	Val	Val	Gly	Gln	Gln	Ala	Thr	Glu	Glu	Met	Leu	Leu	
672		240					245					250					
674	ccc	agg	ttc	ttc	cag	ctg	tgt	tct	gac	aat	gtg	tgg	ggc	gtc	cgg	aag	816
675	Pro	Arg	Phe	Phe	Gln	Leu	Cys	Ser	Asp	Asn	Val	Trp	Gly	Val	Arg	Lys	
676	255				260					265				270			
678	gcc	tgt	gct	gag	tgc	ttc	atg	gcc	gtc	tcc	tgc	gcg	aca	tgc	caa	gaa	864
679	Ala	Cys	Ala	Glu	Cys	Phe	Met	Ala	Val	Ser	Cys	Ala	Thr	Cys	Gln	Glu	
680				275					280					285			
682	atc	cga	cgg	aca	aag	ttg	tca	gca	ctg	ttt	att	aac	ttg	atc	agt	gat	912
683	Ile	Arg	Arg	Thr	Lys	Leu	Ser	Ala	Leu	Phe	Ile	Asn	Leu	Ile	Ser	Asp	
684				290					295					300			
686	cct	tca	cgt	tgg	gtt	cgc	caa	gca	gcc	ttt	cag	tcc	ctg	ggg	cct	ttc	960
687	Pro	Ser	Arg	Trp	Val	Arg	Gln	Ala	Ala	Phe	Gln	Ser	Leu	Gly	Pro	Phe	
688			305					310					315				
690	ata	tcc	aca	ttt	gct	aat	cca	tca	agc	tcg	ggc	cag	tgc	ttc	aaa	gat	1008
691	Ile	Ser	Thr	Phe	Ala	Asn	Pro	Ser	Ser	Ser	Gly	Gln	Cys	Phe	Lys	Asp	
692		320					325					330					
694	gag	agc	aaa	agc	tca	gaa	gac	aaa	gac	agg	atc	aga	gac	gat	ggg	gtt	1056
695	Glu	Ser	Lys	Ser	Ser	Glu	Asp	Lys	Asp	Arg	Ile	Arg	Asp	Asp	Gly	Val	
696	335				340					345				350			
698	gta	caa	gaa	gag	cag	agc	agg	cca	gag	gac	gca	cct	tca	gac	ctc	agt	1104
699	Val	Gln	Glu	Glu	Gln	Ser	Arg	Pro	Glu	Asp	Ala	Pro	Ser	Asp	Leu	Ser	
700				355					360					365			
702	gcc	cct	cac	tcc	agt	gcc	agg	ctg	gac	ggc	aca	ctt	gaa	ggc	tgt	gct	1152

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703	Ala	Pro	His	Ser	Ser	Ala	Arg	Leu	Asp	Gly	Thr	Leu	Glu	Gly	Cys	Ala	
704				370					375					380			
706	gcc	gag	acg	cct	ggg	gac	tct	gca	ggg	gac	atg	cgt	gtt	cca	gcg	gac	1200
707	Ala	Glu	Thr	Pro	Gly	Asp	Ser	Ala	Gly	Asp	Met	Arg	Val	Pro	Ala	Asp	
708				385				390					395				
710	agc	tcc	tta	ctc	tgt	act	ttg	tcc	tca	gag	tct	cct	cag	gaa	gca	gct	1248
711	Ser	Ser	Leu	Leu	Cys	Thr	Leu	Ser	Ser	Glu	Ser	Pro	Gln	Glu	Ala	Ala	
712		400					405					410					
714	agt	gac	gct	gag	agt	ggg	aaa	aag	cac	gat	aac	aac	agc	aag	tct	gcg	1296
715	Ser	Asp	Ala	Glu	Ser	Gly	Lys	Lys	His	Asp	Asn	Asn	Ser	Lys	Ser	Ala	
716	415					420				425						430	
718	tcc	cgg	cca	gac	gtt	ggc	acc	agc	tcc	cca	gag	ccc	act	ccc	tta	gat	1344
719	Ser	Arg	Pro	Asp	Val	Gly	Thr	Ser	Ser	Pro	Glu	Pro	Thr	Pro	Leu	Asp	
720					435					440					445		
722	cag	gaa	atg	ttc	aac	tcc	ttc	cat	ttc	tgg	agg	act	cct	cta	ccc	cag	1392
723	Gln	Glu	Met	Phe	Asn	Ser	Phe	His	Phe	Trp	Arg	Thr	Pro	Leu	Pro	Gln	
724				450					455					460			
726	ata	gat	ctt	gat	aaa	gag	ctc	caa	cag	gac	cct	ggg	gag	agg	ccc	agc	1440
727	Ile	Asp	Leu	Asp	Lys	Glu	Leu	Gln	Gln	Asp	Pro	Gly	Glu	Arg	Pro	Ser	
728			465				470					475					
730	cca	gag	aga	aca	gga	gat	gca	cct	gca	gcc	cct	gta	cca	ggg	tct	ccc	1488
731	Pro	Glu	Arg	Thr	Gly	Asp	Ala	Pro	Ala	Ala	Pro	Val	Pro	Gly	Ser	Pro	
732		480				485						490					
734	agt	atc	acc	atg	gct	acc	cgg	aag	gaa	cta	gaa	gaa	atg	ata	gaa	aac	1536
735	Ser	Ile	Thr	Met	Ala	Thr	Arg	Lys	Glu	Leu	Glu	Glu	Met	Ile	Glu	Asn	
736	495				500					505					510		
738	cta	gag	ccg	cac	atg	gat	gac	ccg	gat	gtt	aaa	gcc	cag	gtg	gaa	gtg	1584
739	Leu	Glu	Pro	His	Met	Asp	Asp	Pro	Asp	Val	Lys	Ala	Gln	Val	Glu	Val	
740				515					520					525			
742	ctg	tcg	gcc	gcc	ctg	cgc	gct	tct	acc	ctg	gat	gct	cac	gac	gag	gct	1632
743	Leu	Ser	Ala	Ala	Leu	Arg	Ala	Ser	Thr	Leu	Asp	Ala	His	Asp	Glu	Ala	
744			530				535					540					
746	ggc	ggg	gca	gag	cag	cgg	agt	gag	ctg	cag	gac	gac	gca	gtg	ggg	gcc	1680
747	Gly	Gly	Ala	Glu	Gln	Arg	Ser	Glu	Leu	Gln	Asp	Asp	Ala	Val	Gly	Ala	
748			545			550						555					
750	ggc	ggc	gag	ctt	cca	aac	tgt	agc	atc	agc	gaa	gac	act	tct	gag	cct	1728
751	Gly	Gly	Glu	Leu	Pro	Asn	Cys	Ser	Ile	Ser	Glu	Asp	Thr	Ser	Glu	Pro	
752		560				565						570					
754	ctg	gtc	atc	gct	gct	gag	gag	aat	atg	gag	gcc	act	cct	gac	tat	atc	1776
755	Leu	Val	Ile	Ala	Ala	Glu	Glu	Asn	Met	Glu	Ala	Thr	Pro	Asp	Tyr	Ile	
756	575				580					585					590		
758	cat	gga	ggg	gcg	gat	gta	ggc	ccc	ggg	ggc	ggg	ggg	ggc	ttc	agc	ccg	1824
759	His	Gly	Gly	Ala	Asp	Val	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Phe	Ser	Pro	
760				595			600					605					
762	gat	gaa	gag	agg	aga	ccc	aaa	gtc	cag	gat	gtc	gta	cca	caa	gcg	tta	1872
763	Asp	Glu	Glu	Arg	Arg	Pro	Lys	Val	Gln	Asp	Val	Val	Pro	Gln	Ala	Leu	
764				610			615					620					
766	cta	gac	cag	tac	ctg	tca	atg	acc	gac	cct	tct	cga	gca	cag	aca	gtc	1920
767	Leu	Asp	Gln	Tyr	Leu	Ser	Met	Thr	Asp	Pro	Ser	Arg	Ala	Gln	Thr	Val	

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768	625	630	635	
770	gac acc gag atc gct aag cac tgt gca tac agt ctg ccg ggt gtg gct	1968		
771	Asp Thr Glu Ile Ala Lys His Cys Ala Tyr Ser Leu Pro Gly Val Ala			
772	640 645 650			
774	ctg acc ctt ggc aga cag aac tgg cac tgc ttg aga gag act tac gag	2016		
775	Leu Thr Leu Gly Arg Gln Asn Trp His Cys Leu Arg Glu Thr Tyr Glu			
776	655 660 665 670			
778	acc cta gcg tca gac atg cag tgg aaa gtt cga aga act ctg gcc ttc	2064		
779	Thr Leu Ala Ser Asp Met Gln Trp Lys Val Arg Arg Thr Leu Ala Phe			
780	675 680 685			
782	tcc atc cat gag ctc gcg gtg att ctc ggg gac cag ctg aca gca gca	2112		
783	Ser Ile His Glu Leu Ala Val Ile Leu Gly Asp Gln Leu Thr Ala Ala			
784	690 695 700			
786	gac ctg gtt ccg att ttt aat ggg ttt tta aaa gat ctt gac gaa gtc	2160		
787	Asp Leu Val Pro Ile Phe Asn Gly Phe Leu Lys Asp Leu Asp Glu Val			
788	705 710 715			
790	agg ata ggt gtt ctc aaa cac ttg cat gac ttt ctg aag ctt ctt cat	2208		
791	Arg Ile Gly Val Leu Lys His Leu His Asp Phe Leu Lys Leu Leu His			
792	720 725 730			
794	att gat aaa aga aga gag tac ctt tat caa ctc cag gag ttt ttg gtg	2256		
795	Ile Asp Lys Arg Arg Glu Tyr Leu Tyr Gln Leu Gln Glu Phe Leu Val			
796	735 740 745 750			
798	aca gac aac agt aga aat tgg cgg ttt cga gct gaa ctg gca gaa cag	2304		
799	Thr Asp Asn Ser Arg Asn Trp Arg Phe Arg Ala Glu Leu Ala Glu Gln			
800	755 760 765			
802	ctg att tta ctt cta gaa tta tat agt ccc aga gat gtt tat gat tac	2352		
803	Leu Ile Leu Leu Leu Glu Leu Tyr Ser Pro Arg Asp Val Tyr Asp Tyr			
804	770 775 780			
806	tta cgt ccc att gct ctg aat ctg tgt gca gac aaa gtt tct tca gtc	2400		
807	Leu Arg Pro Ile Ala Leu Asn Leu Cys Ala Asp Lys Val Ser Ser Val			
808	785 790 795			
810	cgt tgg att tcc tac aag ttg gtc agt gag atg gtg aag cta cac	2448		
811	Arg Trp Ile Ser Tyr Lys Leu Val Ser Glu Met Val Lys Lys Leu His			
812	800 805 810			
814	atg gcg acg ccg cca acg ttc gga gtc gag ctc atc aat gag ctg gtg	2496		
815	Met Ala Thr Pro Pro Thr Phe Gly Val Glu Leu Ile Asn Glu Leu Val			
816	815 820 825 830			
818	gag aac ttc ggc agg tgt cca aag tgg tcg ggc cgg cag gcc ttc gtc	2544		
819	Glu Asn Phe Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln Ala Phe Val			
820	835 840 845			
822	ttc gtg tgc cag act gtc att gag gac gac tgc ctc ccc atg gac cag	2592		
823	Phe Val Cys Gln Thr Val Ile Glu Asp Asp Cys Leu Pro Met Asp Gln			
824	850 855 860			
826	ttt gct gtg cac ctg atg cca cat ttg ctg acc ttg gca aat gac agg	2640		
827	Phe Ala Val His Leu Met Pro His Leu Leu Thr Leu Ala Asn Asp Arg			
828	865 870 875			
830	gtt ccc aac gtt aga gtg ctg ctt gca aaa acc ctt cga cag act cta	2688		
831	Val Pro Asn Val Arg Val Leu Leu Ala Lys Thr Leu Arg Gln Thr Leu			
832	880 885 890			

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834 cta gag aaa gaa tac ttc tta gcc tct gcc agc tgt cat cag gag gcc 2736  
835 Leu Glu Lys Glu Tyr Phe Leu Ala Ser Ala Ser Cys His Gln Glu Ala  
836 895 900 905 910  
838 gtg gag cag aca atc atg gcc ctt cag atg gat cga gac agt gac gtc 2784  
839 Val Glu Gln Thr Ile Met Ala Leu Gln Met Asp Arg Asp Ser Asp Val  
840 915 920 925  
842 aag tac ttt gca agc atc cac ccg tcc agt acc aaa ctc tct gaa gac 2832  
843 Lys Tyr Phe Ala Ser Ile His Pro Ser Ser Thr Lys Leu Ser Glu Asp  
844 930 935 940  
846 gca atg agt aca gct tcc tcc acc tac tga cccctgaccc acggtgtcct 2882  
847 Ala Met Ser Thr Ala Ser Ser Thr Tyr  
848 945 950  
850 tcctgcatcc gcgagagcct ggccctcagcc gectgcgcc ctcgggacag ctgtggtggt 2942  
851 ggggectccc tcctgccagc tcattcgcag gtgcaagttg cctactccca taccagtgtg 3002  
852 tttaagagtc aagagaaagt acagtaaaca ctattatctt atcttgactt agggaaagta 3062  
853 aactctcaga ggattataat tgtcaccaaa gccttaactc attacttcct ctctcgtact 3122  
854 gaatgacttg aattggcaga gcattttccc ttcggaagg aggargttcc cagagacctg 3182  
W--> 855 cgctgctttc tcctgggtttt atttaacgtt ggtaaattggc attcttaccg ccggaagggtg 3242  
856 gacacgcacc ggacagggag gcctgggtat tagcccaagc acttgctcca ggtgcgagtc 3302  
W--> 857 tgctcggctc ntgggctgcc ctgcccagcc ctaagtgtga atagttcttg gcgtgtataa 3362  
W--> 858 atgacaggag tttttcctct cctaagggct tgatgttaac actaagtaga atgtgatttt 3422  
859 gactcctaatt gcagcacatt gctgtacaca ttacagaat gttgcagac tctctcccga 3482  
860 ctcttttcat gctggtcatg acgtgaagg gacttctcag cagatattgt gtcagggtgtt 3542  
861 cttaacttga tcatggtcag ctctgaggtg cgactttcct tcccatgctg cacaccctg 3602  
E--> 862 tggccacgct ggggcatgca gccttaatca tgctgttaga actgttgttg cacaag 3658  
865 <210> SEQ ID NO: 12  
866 <211> LENGTH: 951  
867 <212> TYPE: DNA PRT ←  
868 <213> ORGANISM: RATTUS NORVEGICUS  
870 <400> SEQUENCE: 12  
871 Met Ala Asp Leu Ser Leu Leu Gln Glu Asp Leu Pro Glu Asp Ala Asp  
872 1 5 10 15  
874 Gly Leu Gly Val Asp Asp Tyr Ser Ser Glu Ser Asp Val Ile Ile  
875 20 25 30  
877 Pro Ser Ala Leu Asp Phe Val Ser Gln Asp Glu Met Leu Thr Pro Leu  
878 35 40 45  
880 Gly Arg Leu Asp Lys Tyr Ala Ala Ser Glu Asn Val Phe Asn Arg Gln  
881 50 55 60  
883 Met Val Ala Arg Ser Leu Leu Asp Thr Leu Arg Glu Val Cys Gly Glu  
884 65 70 75 80  
886 Glu Arg Asp Cys Ile Ala Val Leu Glu Arg Ile Ser Arg Leu Ala Asp  
887 85 90 95  
889 Asp Ser Glu Pro Thr Val Arg Ala Glu Leu Met Glu Gln Val Pro His  
890 100 105 110  
892 Ile Ala Leu Phe Cys Gln Glu Asn Arg Pro Ser Ile Pro Tyr Ala Phe  
893 115 120 125  
895 Ser Lys Tyr Leu Leu Pro Ile Val Val Arg Tyr Leu Ala Asp Gln Asn  
896 130 135 140  
898 Asn Gln Val Arg Lys Thr Ser Gln Ala Ala Leu Leu Ala Leu Leu Glu

→ see  
→ item 9  
→ on  
Enon  
summary  
sheet

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/069,439

DATE: 03/07/2002

TIME: 15:26:54

Input Set : A:\2605-103.txt

Output Set: N:\CRF3\03072002\J069439.raw

899	145				150				155				160			
901	Gln	Glu	Leu	Ile	Glu	Arg	Leu	Asp	Val	Glu	Thr	Lys	Val	Cys	Pro	Val
902					165					170					175	
904	Leu	Ile	Asp	Leu	Thr	Ala	Pro	Asp	Ser	Asn	Asp	Asp	Val	Lys	Thr	Glu
905					180					185					190	
907	Ala	Val	Ala	Ile	Met	Cys	Lys	Met	Ala	Pro	Met	Val	Gly	Lys	Asp	Ile
908					195				200					205		
910	Thr	Glu	Arg	Leu	Ile	Leu	Pro	Arg	Phe	Cys	Glu	Met	Cys	Cys	Asp	Cys
911					210				215					220		
913	Arg	Met	Phe	His	Val	Arg	Lys	Val	Cys	Ala	Ala	Asn	Phe	Gly	Asp	Ile
914	225					230					235					240
916	Cys	Ser	Val	Val	Gly	Gln	Gln	Ala	Thr	Glu	Glu	Met	Leu	Leu	Pro	Arg
917					245					250					255	
919	Phe	Phe	Gln	Leu	Cys	Ser	Asp	Asn	Val	Trp	Gly	Val	Arg	Lys	Ala	Cys
920					260					265					270	
922	Ala	Glu	Cys	Phe	Met	Ala	Val	Ser	Cys	Ala	Thr	Cys	Gln	Glu	Ile	Arg
923					275					280				285		
925	Arg	Thr	Lys	Leu	Ser	Ala	Leu	Phe	Ile	Asn	Leu	Ile	Ser	Asp	Pro	Ser
926					290					295				300		
928	Arg	Trp	Val	Arg	Gln	Ala	Ala	Phe	Gln	Ser	Leu	Gly	Pro	Phe	Ile	Ser
929	305					310					315					320
931	Thr	Phe	Ala	Asn	Pro	Ser	Ser	Ser	Gly	Gln	Cys	Phe	Lys	Asp	Glu	Ser
932					325					330					335	
934	Lys	Ser	Ser	Glu	Asp	Lys	Asp	Arg	Ile	Arg	Asp	Asp	Gly	Val	Val	Gln
935					340					345					350	
937	Glu	Glu	Gln	Ser	Arg	Pro	Glu	Asp	Ala	Pro	Ser	Asp	Leu	Ser	Ala	Pro
938					355					360				365		
940	His	Ser	Ser	Ala	Arg	Leu	Asp	Gly	Thr	Leu	Glu	Gly	Cys	Ala	Ala	Glu
941					370					375				380		
943	Thr	Pro	Gly	Asp	Ser	Ala	Gly	Asp	Met	Arg	Val	Pro	Ala	Asp	Ser	Ser
944	385					390					395					400
946	Leu	Leu	Cys	Thr	Leu	Ser	Ser	Glu	Ser	Pro	Gln	Glu	Ala	Ala	Ser	Asp
947					405					410					415	
949	Ala	Glu	Ser	Gly	Lys	Lys	His	Asp	Asn	Asn	Ser	Lys	Ser	Ala	Ser	Arg
950					420					425					430	
952	Pro	Asp	Val	Gly	Thr	Ser	Ser	Pro	Glu	Pro	Thr	Pro	Leu	Asp	Gln	Glu
953					435					440				445		
955	Met	Phe	Asn	Ser	Phe	His	Phe	Trp	Arg	Thr	Pro	Leu	Pro	Gln	Ile	Asp
956					450					455				460		
958	Leu	Asp	Lys	Glu	Leu	Gln	Gln	Asp	Pro	Gly	Glu	Arg	Pro	Ser	Pro	Glu
959	465					470					475					480
961	Arg	Thr	Gly	Asp	Ala	Pro	Ala	Ala	Pro	Val	Pro	Gly	Ser	Pro	Ser	Ile
962					485					490					495	
964	Thr	Met	Ala	Thr	Arg	Lys	Glu	Leu	Glu	Glu	Met	Ile	Glu	Asn	Leu	Glu
965					500					505					510	
967	Pro	His	Met	Asp	Asp	Pro	Asp	Val	Lys	Ala	Gln	Val	Glu	Val	Leu	Ser
968					515					520				525		
970	Ala	Ala	Leu	Arg	Ala	Ser	Thr	Leu	Asp	Ala	His	Asp	Glu	Ala	Gly	Gly
971					530					535				540		



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Input Set : A:\2605-103.txt

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973 Ala Glu Gln Arg Ser Glu Leu Gln Asp Asp Ala Val Gly Ala Gly Gly  
974 545 550 555 560  
976 Glu Leu Pro Asn Cys Ser Ile Ser Glu Asp Thr Ser Glu Pro Leu Val  
977 565 570 575  
979 Ile Ala Ala Glu Asn Met Glu Ala Thr Pro Asp Tyr Ile His Gly  
980 580 585 590  
982 Gly Ala Asp Val Gly Pro Gly Gly Gly Gly Phe Ser Pro Asp Glu  
983 595 600 605  
985 Glu Arg Arg Pro Lys Val Gln Asp Val Val Pro Gln Ala Leu Leu Asp  
986 610 615 620  
988 Gln Tyr Leu Ser Met Thr Asp Pro Ser Arg Ala Gln Thr Val Asp Thr  
989 625 630 635 640  
991 Glu Ile Ala Lys His Cys Ala Tyr Ser Leu Pro Gly Val Ala Leu Thr  
992 645 650 655  
994 Leu Gly Arg Gln Asn Trp His Cys Leu Arg Glu Thr Tyr Glu Thr Leu  
995 660 665 670  
997 Ala Ser Asp Met Gln Trp Lys Val Arg Arg Thr Leu Ala Phe Ser Ile  
998 675 680 685  
1000 His Glu Leu Ala Val Ile Leu Gly Asp Gln Leu Thr Ala Ala Asp Leu  
1001 690 695 700  
1003 Val Pro Ile Phe Asn Gly Phe Leu Lys Asp Leu Asp Glu Val Arg Ile  
1004 705 710 715 720  
1006 Gly Val Leu Lys His Leu His Asp Phe Leu Lys Leu Leu His Ile Asp  
1007 725 730 735  
1009 Lys Arg Arg Glu Tyr Leu Tyr Gln Leu Gln Glu Phe Leu Val Thr Asp  
1010 740 745 750  
1012 Asn Ser Arg Asn Trp Arg Phe Arg Ala Glu Leu Ala Glu Gln Leu Ile  
1013 755 760 765  
1015 Leu Leu Leu Glu Leu Tyr Ser Pro Arg Asp Val Tyr Asp Tyr Leu Arg  
1016 770 775 780  
1018 Pro Ile Ala Leu Asn Leu Cys Ala Asp Lys Val Ser Ser Val Arg Trp  
1019 785 790 795 800  
1021 Ile Ser Tyr Lys Leu Val Ser Glu Met Val Lys Lys Leu His Met Ala  
1022 805 810 815  
1024 Thr Pro Pro Thr Phe Gly Val Glu Leu Ile Asn Glu Leu Val Glu Asn  
1025 820 825 830  
1027 Phe Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln Ala Phe Val Phe Val  
1028 835 840 845  
1030 Cys Gln Thr Val Ile Glu Asp Asp Cys Leu Pro Met Asp Gln Phe Ala  
1031 850 855 860  
1033 Val His Leu Met Pro His Leu Leu Thr Leu Ala Asn Asp Arg Val Pro  
1034 865 870 875 880  
1036 Asn Val Arg Val Leu Leu Ala Lys Thr Leu Arg Gln Thr Leu Leu Glu  
1037 885 890 895  
1039 Lys Glu Tyr Phe Leu Ala Ser Ala Ser Cys His Gln Glu Ala Val Glu  
1040 900 905 910  
1042 Gln Thr Ile Met Ala Leu Gln Met Asp Arg Asp Ser Asp Val Lys Tyr  
1043 915 920 925  
1045 Phe Ala Ser Ile His Pro Ser Ser Thr Lys Leu Ser Glu Asp Ala Met

RAW SEQUENCE LISTING

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Input Set : A:\2605-103.txt

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1046	930	935	940
1048	Ser Thr Ala Ser Ser Thr Tyr		
E--> 1049	945	950	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/069,439

DATE: 03/07/2002

TIME: 15:26:56

Input Set : A:\2605-103.txt

Output Set: N:\CRF3\03072002\J069439.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:855 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
 L:855 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:3182  
 L:857 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
 L:857 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:3302  
 L:858 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
 L:858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:3362  
 L:862 M:252 E: No. of Seq. differs, <211> LENGTH:Input:3568 Found:3658 SEQ:11  
 L:1049 M:252 E: No. of Seq. differs, <211> LENGTH:Input:951 Found:0 SEQ:12